

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT:
  - (A) NAME: ASTRA AB
  - (B) STREET: Västra Mälarehamnen 9
  - (C) CITY: Södertälje
  - (E) COUNTRY: Sweden
  - (F) POSTAL CODE (ZIP): S-151 85
  - (G) TELEPHONE: +46-8-553 260 00
  - (H) TELEFAX: +46-8-553 288 20
  - (I) TELEX: 19237 astra s
- (ii) TITLE OF INVENTION: DNA Sequences for Expression of Polypeptides
- (iii) NUMBER OF SEQUENCES: 4
- (iv) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release 1.0, Version 1.30 (EPO)

## (2) INFORMATION FOR SEQ ID NC: 1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2428 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
  - (F) TISSUE TYPE: mammary gland
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 82..2319
  - (D) OTHER INFORMATION:/product= "bile-salt-stimulated lipase"
- (ix) FEATURE:
  - (A) NAME/KEY: exon
  - (B) LOCATION: 985..1173
- (ix) FEATURE:
  - (A) NAME/KEY: exon
  - (B) LOCATION: 1174..1377
- (ix) FEATURE:
  - (A) NAME/KEY: exon
  - (B) LOCATION: 1378..1575
- (ix) FEATURE:
  - (A) NAME/KEY: exon
  - (B) LOCATION: 1576..2415

- (ix) FEATURE:
  - (A) NAME/KEY: mat\_peptide
  - (B) LOCATION:151..2316
- (ix) FEATURE:
  - (A) NAME/KEY: polyA\_signal
  - (B) LOCATION:2397..2402
- (ix) FEATURE:
  - (A) NAME/KEY: repeat\_region
  - (B) LOCATION:1756..2283
- (ix) FEATURE:
  - (A) NAME/KEY: 5'UTR
  - (B) LOCATION:1..81
- (ix) FEATURE:
  - (A) NAME/KEY: repeat\_unit
  - (B) LOCATION:1756..1788
- (ix) FEATURE:
  - (A) NAME/KEY: repeat\_unit
  - (B) LOCATION:1789..1821
- (ix) FEATURE:
  - (A) NAME/KEY: repeat\_unit
  - (B) LOCATION:1822..1854
- (ix) FEATURE:
  - (A) NAME/KEY: repeat\_unit
  - (B) LOCATION:1855..1887
- (ix) FEATURE:
  - (A) NAME/KEY: repeat\_unit
  - (B) LOCATION:1888..1920
- (ix) FEATURE:
  - (A) NAME/KEY: repeat\_unit
  - (B) LOCATION:1921..1953
- (ix) FEATURE:
  - (A) NAME/KEY: repeat\_unit
  - (B) LOCATION:1954..1986
- (ix) FEATURE:
  - (A) NAME/KEY: repeat\_unit
  - (B) LOCATION:1987..2019
- (ix) FEATURE:
  - (A) NAME/KEY: repeat\_unit
  - (B) LOCATION:2020..2052
- (ix) FEATURE:
  - (A) NAME/KEY: repeat\_unit
  - (B) LOCATION:2053..2085
- (ix) FEATURE:
  - (A) NAME/KEY: repeat\_unit
  - (B) LOCATION:2086..2118
- (ix) FEATURE:
  - (A) NAME/KEY: repeat\_unit
  - (B) LOCATION:2119..2151
- (ix) FEATURE:
  - (A) NAME/KEY: repeat\_unit
  - (B) LOCATION:2152..2184

(ix) FEATURE:

(A) NAME/KEY: repeat\_unit  
(B) LOCATION:2185..2217

(ix) FEATURE:

(A) NAME/KEY: repeat\_unit  
(B) LOCATION:2218..2250

( ix ) FEATURE :

- (A) NAME/KEY: repeat\_unit
- (B) LOCATION:2251..2283

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Nilsson, Jeanette  
Bläckberg, Lars  
Carlsson, Peter  
Enerbäck, Sven  
Hernell, Olle  
Bjursell, Gunnar

(B) TITLE: cDNA cloning of human-milk

(B) Title: *Chen et al. (1979) bile-salt-stimulated lipase and evidence for its identity to pancreatic carboxylic ester hydrolase*

(C) JOURNAL: Eur. J. Biochem.

(D) VOLUME: 192

(F) PAGES: 543-550

(G) DATE: Sept. - 1990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ACCTTCTGTA TCAGTTAAGT GTCAAGATGG AAGAACAGC AGTCTCAAGA TAATGCAAAG	60
AGTTTATTCA TCCAGAGGCT G ATG CTC ACC ATG GGG CGC CTG CAA CTG GTT	111
Met Leu Thr Met Gly Arg Leu Gln Leu Val	
-23 -20 -15	
GTG TTG GGC CTC ACC TGC TGC TGG GCA GTG GCG AGT GCC GCG AAG CTG	159
Val Leu Gly Leu Thr Cys Cys Trp Ala Val Ala Ser Ala Ala Lys Leu	
-10 -5 1	
GGC GCC GTG TAC ACA GAA GGT GGG TTC GTG CAA GGC GTC AAT AAG AAG	207
Gly Ala Val Tyr Thr Glu Gly Gly Phe Val Glu Gly Val Asn Lys Lys	
5 10 15	
CTC CGC CTC CTG GGT GAC TCT GTG GAC ATC TTC AAG GGC ATC CCC TTC	255
Leu Gly Leu Leu Gly Asp Ser Val Asp Ile Phe Lys Gly Ile Pro Phe	
20 25 30 35	
GCA GCT CCC ACC AAG GCC CTG GAA AAT CCT CAG CCA CAT CCT GGC TGG	303
Ala Ala Pro Thr Lys Ala Leu Glu Asn Pro Gln Pro His Pro Trp	
40 45 50	
CAA GGG ACC CTG AAG GCC AAG AAC TTC AAG AAG AGA TGC CTG CAG GCC	351
Gln Gly Thr Leu Lys Ala Lys Asn Phe Lys Lys Arg Cys Leu Gln Ala	
55 60 65	
ACC ATC ACC CAG GAC AGC ACC TAC GGG GAT GAA GAC TGC CTG TAC CTC	399
Thr Ile Thr Gln Asp Ser Thr Tyr Gly Asp Glu Asp Cys Leu Tyr Leu	
70 75 80	
AAC ATT TGG GTG CCC CAG GGC AGG AAG CAA GTC TCC CGG GAC CTG CCC	441
Asn Ile Trp Val Pro Gln Gly Arg Lys Gln Val Ser Arg Asp Leu Pro	
85 90 95	
GTT ATG ATC TGG ATC TAT GGA GGC GCC TTC CTC ATG GGG TCC GGC CAT	491
Val Met Ile Trp Ile Tyr Gly Gly Ala Phe Leu Met Gly Ser Gly His	
100 105 110 115	

GGG GCC AAC TTC CTC AAC AAC TAC CTG TAT GAC GGC GAG GAG ATC GCC Gly Ala Asn Phe Leu Asn Asn Tyr Leu Tyr Asp Gly Glu Glu Ile Ala 120 125 130	543
ACA CGC GGA AAC GTC ATC GTG GTC ACC TTC AAC TAC CGT GTC GGC CCC Thr Arg Gly Asn Val Ile Val Val Thr Phe Asn Tyr Arg Val Gly Pro 135 140 145	591
CTT GGG TTC CTC AGC ACT GGG GAC GCC AAT CTG CCA GGT AAC TAT GGC Leu Gly Phe Leu Ser Thr Gly Asp Ala Asn Leu Pro Gly Asn Tyr Gly 150 155 160	639
CTT CGG GAT CAG CAC ATG GCC ATT GCT TGG GTG AAG AGG AAT ATC GCG Leu Arg Asp Gln His Met Ala Ile Ala Trp Val Lys Arg Asn Ile Ala 165 170 175	687
GCC TTC GGG GGG GAC CCC AAC AAC ATC ACG CTC TTC GGG GAG TCT GCT Ala Phe Gly Gly Asp Pro Asn Asn Ile Thr Leu Phe Gly Glu Ser Ala 180 185 190 195	735
GGA GGT GCC AGC GTC TCT CTG CAG ACC CTC TCC CCC TAC AAC AAG GGC Gly Gly Ala Ser Val Ser Leu Gln Thr Leu Ser Pro Tyr Asn Lys Gly 200 205 210	783
CTC ATC CGG CGA GCC ATC AGC CAG AGC GGC GTG GCC CTG AGT CCC TGG Leu Ile Arg Arg Ala Ile Ser Gln Ser Gly Val Ala Leu Ser Pro Trp 215 220 225	831
GTC ATC CAG AAA AAC CCA CTC TTC TGG GCC AAA AAG GTG GCT GAG AAG Val Ile Gln Lys Asn Pro Leu Phe Trp Ala Lys Val Ala Glu Lys 230 235 240	879
GTG GGT TGC CCT GTG GGT GAT GCC GCC AGG ATG GCC CAG TGT CTG AAG Val Gly Cys Pro Val Gly Asp Ala Ala Arg Met Ala Gln Cys Leu Lys 245 250 255	927
GTT ACT GAT CCC CGA GCC CTG ACG CTG GCC TAT AAG GTG CCG CTG GCA Val Thr Asp Pro Arg Ala Leu Thr Leu Ala Tyr Lys Val Pro Leu Ala 260 265 270 275	975
GGC CTG GAG TAC CCC ATG CTG CAC TAT GTG GGC TTC GTC CCT GTC ATT Gly Leu Glu Tyr Pro Met Leu His Tyr Val Gly Phe Val Pro Val Ile 280 285 290	1023
GAT GGA GAC TTC ATC CCC GCT GAC CCG ATC AAC CTG TAC GCC AAC GCC Asp Gly Asp Phe Ile Pro Ala Asp Pro Ile Asn Leu Tyr Ala Asn Ala 295 300 305	1071
GCC GAC ATC GAC TAT ATA GCA GGC ACC AAC AAC ATG GAC GGC CAC ATC Ala Asp Ile Asp Tyr Ile Ala Gly Thr Asn Asn Met Asp Gly His Ile 310 315 320	1119
TTC GCC AGC ATC GAC ATG CCT GCC ATC AAC AAG GGC AAC AAG AAA GTC Phe Ala Ser Ile Asp Met Pro Ala Ile Asn Lys Gly Asn Lys Lys Val 325 330 335	1167
ACG GAG GAG GAC TTC TAC AAG CTG GTC AGT GAG TTC ACA ATC ACC AAG Thr Glu Glu Asp Phe Tyr Lys Leu Val Ser Glu Phe Thr Ile Thr Lys 340 345 350 355	1215
GGG CTC AGA GGC GCC AAG ACG ACC TTT GAT GTC TAC ACC GAG TCC TGG Gly Leu Arg Gly Ala Lys Thr Thr Phe Asp Val Tyr Thr Glu Ser Trp 360 365 370	1263
GCC CAG GAC CCA TCC CAG GAG AAT AAG AAG AAG ACT GTG GTG GAC TTT Ala Gln Asp Pro Ser Gln Glu Asn Lys Lys Lys Thr Val Val Asp Phe 375 380 385	1311

GAG ACC GAT GTC CTC TTC CTG GTG CCC ACC GAG ATT GCC CTA GCC CAG Glu Thr Asp Val Leu Phe Leu Val Pro Thr Glu Ile Ala Leu Ala Gln 390	395	400	1359	
CAC AGA GCC AAT GCC AAG AGT GCC AAG ACC TAC GCC TAC CTG TTT TCC His Arg Ala Asn Ala Lys Ser Ala Lys Thr Tyr Ala Tyr Leu Phe Ser 405	410	415	1407	
CAT CCC TCT CGG ATG CCC GTC TAC CCC AAA TGG GTG GGG GCC GAC CAT His Pro Ser Arg Met Pro Val Tyr Pro Lys Trp Val Gly Ala Asp His 420	425	430	435	1455
GCA GAT GAC ATT CAG TAC GTT TTC GGG AAG CCC TTC GCC ACC CCC ACG Ala Asp Asp Ile Gln Tyr Val Phe Gly Lys Pro Phe Ala Thr Pro Thr 440	445	450	455	1503
GGC TAC CGG CCC CAA GAC AGG ACA GTC TCT AAG GCC ATG ATC GCC TAC Gly Tyr Arg Pro Gln Asp Arg Thr Val Ser Lys Ala Met Ile Ala Tyr 455	460	465	470	1551
TGG ACC AAC TTT GCC AAA ACA GGG GAC CCC AAC ATG GGC GAC TCG GCT Trp Thr Asn Phe Ala Lys Thr Gly Asp Pro Asn Met Gly Asp Ser Ala 470	475	480	485	1599
GTG CCC ACA CAC TGG GAA CCC TAC ACT ACG GAA AAC AGC GGC TAC CTG Val Pro Thr His Trp Glu Pro Tyr Thr Thr Glu Asn Ser Gly Tyr Leu 485	490	495	500	1647
GAG ATC ACC AAG AAG ATG GGC AGC AGC TCC ATG AAG GGG AGC CTG AGA Glu Ile Thr Lys Lys Met Gly Ser Ser Met Lys Arg Ser Leu Arg 500	505	510	515	1695
ACC AAC TTC CTG CGC TAC TGG ACC CTC ACC TAT CTG GGG CTG CCC ACA Thr Asn Phe Leu Arg Tyr Trp Thr Leu Thr Tyr Leu Ala Leu Pro Thr 520	525	530	535	1743
GTG ACC GAC CAG GAG GCC ACC CCT GTG CCC CCC ACA GGG GAC TCC GAG Val Thr Asp Gln Glu Ala Thr Pro Val Pro Pro Thr Gly Asp Ser Glu 535	540	545	550	1791
GCC ACT CCC GTG CCC CCC ACG GGT GAC TCC GAG ACC GCC CCC GTG CCG Ala Thr Pro Val Pro Pro Thr Gly Asp Ser Glu Thr Ala Pro Val Pro 550	555	560	565	1839
CCC ACG GGT GAC TCC GGG GCC CCC CCC GTG CCG CCC ACG GGT GAC TCC Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser 565	570	575	580	1887
GGG GCC CCC CCC GTG CCG CCC ACG GGT GAC TCC GGG GCC CCC CCC GTG Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val 580	585	590	595	1935
CCG CCC ACG GGT GAC TCC GGG GCC CCC CCC GTG CCG CCC ACG GGT GAC Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp 600	605	610	615	1983
TCC GGG GCC CCC CCC GTG CCG CCC ACG GGT GAC TCC GGG GCC CCC CCC Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro 615	620	625	630	2031
GTG CCG CCC ACG GGT GAC TCC GGG GCC CCC CCC GTG CCG CCC ACG GGT Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly 630	635	640	645	2079
GAC GCC GGG CCC CCC CCC GTG CCG CCC ACG GGT GAC TCC GGG GCC CCC Asp Ala Gly Pro Pro Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro 645	650	655	660	2127

CCC GTG CCG CCC ACG GGT GAC TCC GGG GCC CCC CCC GTG ACC CCC ACG	2175
Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Thr Pro Thr	
660 665 670 675	
GGT GAC TCC GAG ACC GCC CCC GTG CCG CCC ACG GGT GAC TCC GGG GCC	2223
Gly Asp Ser Glu Thr Ala Pro Val Pro Pro Thr Gly Asp Ser Gly Ala	
680 685 690	
CCC CCT GTG CCC CCC ACG GGT GAC TCT GAG GCT GCC CCT GTG CCC CCC	2271
Pro Pro Val Pro Pro Thr Gly Asp Ser Glu Ala Ala Pro Val Pro Pro	
695 700 705	
ACA GAT GAC TCC AAG GAA GCT CAG ATG CCT GCA GTC ATT AGG TTT TAG	2319
Thr Asp Asp Ser Lys Glu Ala Gln Met Pro Ala Val Ile Arg Phe *	
710 715 720	
CGTCCCCATGA GCCTTGGTAT CAAGAGGCCA CAAGAGTGGG ACCCCAGGGG CTCCCCCTCCC	2379
ATCTTGAGCT CTTCCTGAAT AAAGCCTCAT ACCCCTAAAAA AAAAALAAA	.2428

## (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 746 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Leu Thr Met Gly Arg Leu Gln Leu Val Val Leu Gly Leu Thr Cys	
-23 -20 -15 -10	
Cys Trp Ala Val Ala Ser Ala Ala Lys Leu Gly Ala Val Tyr Thr Glu	
-5 1 5	
Gly Gly Phe Val Glu Gly Val Asn Lys Lys Leu Gly Leu Leu Gly Asp	
10 15 20 25	
Ser Val Asp Ile Phe Lys Gly Ile Pro Phe Ala Ala Pro Thr Lys Ala	
30 35 40	
Leu Glu Asn Pro Gln Pro His Pro Gly Trp Gln Gly Thr Leu Lys Ala	
45 50 55	
Lys Asn Phe Lys Lys Arg Cys Leu Gln Ala Thr Ile Thr Gln Asp Ser	
60 65 70	
Thr Tyr Gly Asp Glu Asp Cys Leu Tyr Leu Asn Ile Trp Val Pro Gln	
75 80 85	
Gly Arg Lys Gln Val Ser Arg Asp Leu Pro Val Met Ile Trp Ile Tyr	
90 95 100 105	
Gly Gly Ala Phe Leu Met Gly Ser Gly His Gly Ala Asn Phe Leu Asn	
110 115 120	
Asn Tyr Leu Tyr Asp Gly Glu Ile Ala Thr Arg Gly Asn Val Ile	
125 130 135	
Val Val Thr Phe Asn Tyr Arg Val Gly Pro Leu Gly Phe Leu Ser Thr	
140 145 150	
Gly Asp Ala Asn Leu Pro Gly Asn Tyr Gly Leu Arg Asp Gln His Met	
155 160 165	

Ala Ile Ala Trp Val Lys Arg Asn Ile Ala Ala Phe Gly Gly Asp Pro  
 170 175 180 185  
 Asn Asn Ile Thr Leu Phe Gly Glu Ser Ala Gly Gly Ala Ser Val Ser  
 190 195 200  
 Leu Gln Thr Leu Ser Pro Tyr Asn Lys Gly Leu Ile Arg Arg Ala Ile  
 205 210 215  
 Ser Gln Ser Gly Val Ala Leu Ser Pro Trp Val Ile Gln Lys Asn Pro  
 220 225 230  
 Leu Phe Trp Ala Lys Lys Val Ala Glu Lys Val Gly Cys Pro Val Gly  
 235 240 245  
 Asp Ala Ala Arg Met Ala Gln Cys Leu Lys Val Thr Asp Pro Arg Ala  
 250 255 260 265  
 Leu Thr Leu Ala Tyr Lys Val Pro Leu Ala Gly Leu Glu Tyr Pro Met  
 270 275 280  
 Leu His Tyr Val Gly Phe Val Pro Val Ile Asp Gly Asp Phe Ile Pro  
 285 290 295  
 Ala Asp Pro Ile Asn Leu Tyr Ala Asn Ala Asp Ile Asp Tyr Ile  
 300 305 310  
 Ala Gly Thr Asn Asn Met Asp Gly His Ile Phe Ala Ser Ile Asp Met  
 315 320 325  
 Pro Ala Ile Asn Lys Gly Asn Lys Lys Val Thr Glu Glu Asp Phe Tyr  
 330 335 340 345  
 Lys Leu Val Ser Glu Phe Thr Ile Thr Lys Gly Leu Arg Gly Ala Lys  
 350 355 360  
 Thr Thr Phe Asp Val Tyr Thr Glu Ser Trp Ala Gln Asp Pro Ser Gln  
 365 370 375  
 Glu Asn Lys Lys Lys Thr Val Val Asp Phe Glu Thr Asp Val Leu Phe  
 380 385 390  
 Leu Val Pro Thr Glu Ile Ala Leu Ala Gln His Arg Ala Asn Ala Lys  
 395 400 405  
 Ser Ala Lys Thr Tyr Ala Tyr Leu Phe Ser His Pro Ser Arg Met Pro  
 410 415 420 425  
 Val Tyr Pro Lys Trp Val Gly Ala Asp His Ala Asp Asp Ile Gln Tyr  
 430 435 440  
 Val Phe Gly Lys Pro Phe Ala Thr Pro Thr Gly Tyr Arg Pro Gln Asp  
 445 450 455  
 Arg Thr Val Ser Lys Ala Met Ile Ala Tyr Trp Thr Asn Phe Ala Lys  
 460 465 470  
 Thr Gly Asp Pro Asn Met Gly Asp Ser Ala Val Pro Thr His Trp Glu  
 475 480 485  
 Pro Tyr Thr Thr Glu Asn Ser Gly Tyr Leu Glu Ile Thr Lys Lys Met  
 490 495 500 505  
 Gly Ser Ser Ser Met Lys Arg Ser Leu Arg Thr Asn Phe Leu Arg Tyr  
 510 515 520  
 Trp Thr Leu Thr Tyr Leu Ala Leu Pro Thr Val Thr Asp Gln Glu Ala  
 525 530 535

Thr Pro Val Pro Pro Thr Gly Asp Ser Glu Ala Thr Pro Val Pro Pro  
 540 545 550  
 Thr Gly Asp Ser Glu Thr Ala Pro Val Pro Pro Thr Gly Asp Ser Gly  
 555 560 565  
 Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro  
 570 575 580 585  
 Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser  
 590 595 600  
 Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val  
 605 610 615  
 Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp  
 620 625 630  
 Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ala Gly Pro Pro Pro  
 635 640 645  
 Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly  
 650 655 660 665  
 Asp Ser Gly Ala Pro Pro Val Thr Pro Thr Gly Asp Ser Glu Thr Ala  
 670 675 680  
 Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr  
 685 690 695  
 Gly Asp Ser Glu Ala Ala Pro Val Pro Pro Thr Asp Asp Ser Lys Glu  
 700 705 710  
 Ala Gln Met Pro Ala Val Ile Arg Phe \*  
 715 720

## (2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 722 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
  - (F) TISSUE TYPE: Mammary gland

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Ala Lys Leu Gly Ala Val Tyr Thr Glu Gly Gly Phe Val Glu Gly Val  
 1 5 10 15  
 Asn Lys Lys Leu Gly Leu Leu Gly Asp Ser Val Asp Ile Phe Lys Gly  
 20 25 30  
 Ile Pro Phe Ala Ala Pro Thr Lys Ala Leu Glu Asn Pro Gln Pro His  
 35 40 45  
 Pro Gly Trp Gln Gly Thr Leu Lys Ala Lys Asn Phe Lys Lys Arg Cys  
 50 55 60

Leu Gln Ala Thr Ile Thr Gln Asp Ser Thr Tyr Gly Asp Glu Asp Cys  
 65 70 75 80  
 Leu Tyr Leu Asn Ile Trp Val Pro Gln Gly Arg Lys Gln Val Ser Arg  
 85 90 95  
 Asp Leu Pro Val Met Ile Trp Ile Tyr Gly Gly Ala Phe Leu Met Gly  
 100 105 110  
 Ser Gly His Gly Ala Asn Phe Leu Asn Asn Tyr Leu Tyr Asp Gly Glu  
 115 120 125  
 Glu Ile Ala Thr Arg Gly Asn Val Ile Val Val Thr Phe Asn Tyr Arg  
 130 135 140  
 Val Gly Pro Leu Gly Phe Leu Ser Thr Gly Asp Ala Asn Leu Pro Gly  
 145 150 155 160  
 Asn Tyr Gly Leu Arg Asp Gln His Met Ala Ile Ala Trp Val Lys Arg .  
 165 170 175  
 Asn Ile Ala Ala Phe Gly Gly Asp Pro Asn Asn Ile Thr Leu Phe Gly  
 180 185 190  
 Glu Ser Ala Gly Gly Ala Ser Val Ser Leu Gln Thr Leu Ser Pro Tyr  
 195 200 205  
 Asn Lys Gly Leu Ile Arg Arg Ala Ile Ser Gln Ser Gly Val Ala Leu  
 210 215 220  
 Ser Pro Trp Val Ile Gln Lys Asn Pro Leu Phe Trp Ala Lys Lys Val  
 225 230 235 240  
 Ala Glu Lys Val Gly Cys Pro Val Gly Asp Ala Ala Arg Met Ala Gln  
 245 250 255  
 Cys Leu Lys Val Thr Asp Pro Arg Ala Leu Thr Leu Ala Tyr Lys Val  
 260 265 270  
 Pro Leu Ala Gly Leu Glu Tyr Pro Met Leu His Tyr Val Gly Phe Val  
 275 280 285  
 Pro Val Ile Asp Gly Asp Phe Ile Pro Ala Asp Pro Ile Asn Leu Tyr  
 290 295 300  
 Ala Asn Ala Ala Asp Ile Asp Tyr Ile Ala Gly Thr Asn Asn Met Asp  
 305 310 315 320  
 Gly His Ile Phe Ala Ser Ile Asp Met Pro Ala Ile Asn Lys Gly Asn  
 325 330 335  
 Lys Lys Val Thr Glu Glu Asp Phe Tyr Lys Leu Val Ser Glu Phe Thr  
 340 345 350  
 Ile Thr Lys Gly Leu Arg Gly Ala Lys Thr Thr Phe Asp Val Tyr Thr  
 355 360 365  
 Glu Ser Trp Ala Gln Asp Pro Ser Gln Glu Asn Lys Lys Lys Thr Val  
 370 375 380  
 Val Asp Phe Glu Thr Asp Val Leu Phe Leu Val Pro Thr Glu Ile Ala  
 385 390 395 400  
 Leu Ala Gln His Arg Ala Asn Ala Lys Ser Ala Lys Thr Tyr Ala Tyr  
 405 410 415  
 Leu Phe Ser His Pro Ser Arg Met Pro Val Tyr Pro Lys Trp Val Gly  
 420 425 430

Ala Asp His Ala Asp Asp Ile Gln Tyr Val Phe Gly Lys Pro Phe Ala  
 435 440 445  
 Thr Pro Thr Gly Tyr Arg Pro Gln Asp Arg Thr Val Ser Lys Ala Met  
 450 455 460  
 Ile Ala Tyr Trp Thr Asn Phe Ala Lys Thr Gly Asp Pro Asn Met Gly  
 465 470 475 480  
 Asp Ser Ala Val Pro Thr His Trp Glu Pro Tyr Thr Thr Glu Asn Ser  
 485 490 495  
 Gly Tyr Leu Glu Ile Thr Lys Lys Met Gly Ser Ser Ser Met Lys Arg  
 500 505 510  
 Ser Leu Arg Thr Asn Phe Leu Arg Tyr Trp Thr Leu Thr Tyr Leu Ala  
 515 520 525  
 Leu Pro Thr Val Thr Asp Gln Glu Ala Thr Pro Val Pro Pro Thr Gly  
 530 535 540  
 Asp Ser Glu Ala Thr Pro Val Pro Pro Thr Gly Asp Ser Glu Thr Ala  
 545 550 555 560  
 Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr  
 565 570 575  
 Gly Asp Ser Gly Ala Pro Pro Val Prc Pro Thr Gly Asp Ser Gly Ala  
 580 585 590  
 Pro Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro  
 595 600 605  
 Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Gly  
 610 615 620  
 Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro  
 625 630 635 640  
 Pro Thr Gly Asp Ala Gly Pro Pro Prc Val Pro Pro Thr Gly Asp Ser  
 645 650 655  
 Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val  
 660 665 670  
 Thr Pro Thr Gly Asp Ser Glu Thr Ala Pro Val Pro Pro Thr Gly Asp  
 675 680 685  
 Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Glu Ala Ala Pro  
 690 695 700  
 Val Pro Pro Thr Asp Asp Ser Lys Glu Ala Gln Met Pro Ala Val Ile  
 705 710 715 720  
 Arg Phe

## (2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 568 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens  
(F) TISSUE TYPE: Mammary gland

(ix) FEATURE:

(A) NAME/KEY: Peptide  
(B) LOCATION: 1..568  
(D) OTHER INFORMATION: /label= Variant\_C

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Hansson, Lennart  
Blackberg, Lars  
Edlund, Michael  
Lundberg, Lennart  
Stromqvist, Mats  
Hernell, Olle(B) TITLE: Recombinant Human Milk Bile Salt-stimulated  
Lipase(C) JOURNAL: J. Biol. Chem.  
(D) VOLUME: 268  
(E) ISSUE: 35  
(F) PAGES: 26692-26698  
(G) DATE: Dec. 15-1993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Ala Lys Leu Gly Ala Val Tyr Thr Glu Gly Gly Phe Val Glu Gly Val  
1 5 10 15Asn Lys Lys Leu Gly Leu Leu Gly Asp Ser Val Asp Ile Phe Lys Gly  
20 25 30Ile Pro Phe Ala Ala Pro Thr Lys Ala Leu Glu Asn Pro Gln Pro His  
35 40 45Pro Gly Trp Gln Gly Thr Leu Lys Ala Lys Asn Phe Lys Lys Arg Cys  
50 55 60Leu Gln Ala Thr Ile Thr Gln Asp Ser Thr Tyr Gly Asp Glu Asp Cys  
65 70 75 80Leu Tyr Leu Asn Ile Trp Val Pro Gln Gly Arg Lys Gln Val Ser Arg  
85 90 95Asp Leu Pro Val Met Ile Trp Ile Tyr Gly Gly Ala Phe Leu Met Gly  
100 105 110Ser Gly His Gly Ala Asn Phe Leu Asn Asn Tyr Leu Tyr Asp Gly Glu  
115 120 125Glu Ile Ala Thr Arg Gly Asn Val Ile Val Val Thr Phe Asn Tyr Arg  
130 135 140Val Gly Pro Leu Gly Phe Leu Ser Thr Gly Asp Ala Asn Leu Pro Gly  
145 150 155 160Asn Tyr Gly Leu Arg Asp Gln His Met Ala Ile Ala Trp Val Lys Arg  
165 170 175Asn Ile Ala Ala Phe Gly Asp Pro Asn Asn Ile Thr Leu Phe Gly  
180 185 190Glu Ser Ala Gly Gly Ala Ser Val Ser Leu Gln Thr Leu Ser Pro Tyr  
195 200 205

Asn Lys Gly Leu Ile Arg Arg Ala Ile Ser Gln Ser Gly Val Ala Leu  
 210 215 220  
 Ser Pro Trp Val Ile Gln Lys Asn Pro Leu Phe Trp Ala Lys Lys Val  
 225 230 235 240  
 Ala Glu Lys Val Gly Cys Pro Val Gly Asp Ala Ala Arg Met Ala Gln  
 245 250 255  
 Cys Leu Lys Val Thr Asp Pro Arg Ala Leu Thr Leu Ala Tyr Lys Val  
 260 265 270  
 Pro Leu Ala Gly Leu Glu Tyr Pro Met Leu His Tyr Val Gly Phe Val  
 275 280 285  
 Pro Val Ile Asp Gly Asp Phe Ile Pro Ala Asp Pro Ile Asn Leu Tyr  
 290 295 300  
 Ala Asn Ala Ala Asp Ile Asp Tyr Ile Ala Gly Thr Asn Asn Met Asp  
 305 310 315 320  
 Gly His Ile Phe Ala Ser Ile Asp Met Pro Ala Ile Asn Lys Gly Asn  
 325 330 335  
 Lys Lys Val Thr Glu Glu Asp Phe Tyr Lys Leu Val Ser Glu Phe Thr  
 340 345 350  
 Ile Thr Lys Gly Leu Arg Gly Ala Lys Thr Thr Phe Asp Val Tyr Thr  
 355 360 365  
 Glu Ser Trp Ala Gln Asp Pro Ser Gln Glu Asn Lys Lys Lys Thr Val  
 370 375 380  
 Val Asp Phe Glu Thr Asp Val Leu Phe Leu Val Pro Thr Glu Ile Ala  
 385 390 395 400  
 Leu Ala Gln His Arg Ala Asn Ala Lys Ser Ala Lys Thr Tyr Ala Tyr  
 405 410 415  
 Leu Phe Ser His Pro Ser Arg Met Pro Val Tyr Pro Lys Trp Val Gly  
 420 425 430  
 Ala Asp His Ala Asp Asp Ile Gln Tyr Val Phe Gly Lys Pro Phe Ala  
 435 440 445  
 Thr Pro Thr Gly Tyr Arg Pro Gln Asp Arg Thr Val Ser Lys Ala Met  
 450 455 460  
 Ile Ala Tyr Trp Thr Asn Phe Ala Lys Thr Gly Asp Pro Asn Met Gly  
 465 470 475 480  
 Asp Ser Ala Val Pro Thr His Trp Glu Pro Tyr Thr Thr Glu Asn Ser  
 485 490 495  
 Gly Tyr Leu Glu Ile Thr Lys Lys Met Gly Ser Ser Ser Met Lys Arg  
 500 505 510  
 Ser Leu Arg Thr Asn Phe Leu Arg Tyr Trp Thr Leu Thr Tyr Leu Ala  
 515 520 525  
 Leu Pro Thr Val Thr Asp Gln Gly Ala Pro Pro Val Pro Pro Thr Gly  
 530 535 540  
 Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Lys Glu Ala  
 545 550 555 560  
 Gln Met Pro Ala Val Ile Arg Phe  
 565

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No.

## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

**A.** The indications made below relate to the microorganism referred to in the description  
on page 9, line 8.

**B. IDENTIFICATION OF DEPOSIT**

Further deposits are identified on an additional sheet

Name of depositary institution

The National Collections of Industrial and Marine Bacteria Limited (NCIMB)

Address of depositary institution (including postal code and country)

23 St Machar Drive  
Aberdeen AB2 1RY  
Scotland, UK

Date of deposit

2 May 1995

Accession Number

NCIMB 40721

**C. ADDITIONAL INDICATIONS** (leave blank if not applicable)

This information is continued on an additional sheet

In respect of all designated states in which such action is possible and to the extent that it is legally permissible under the law of the designated state, it is requested that a sample of the deposited micro-organism be made available only by the issue thereof to an independent expert, in accordance with the relevant patent legislation, e.g. Rule 28(4) EPC, and generally similar provisions *mutatis mutandis* for any other designated state.

**D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE** (if the indications are not for all designated States)

**E. SEPARATE FURNISHING OF INDICATIONS** (leave blank if not applicable)

The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")

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International application to.

## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description  
12 on page \_\_\_\_\_, line \_\_\_\_\_ 19-20

## B. IDENTIFICATION OF DEPOSIT

Further deposits are identified on an additional sheet 

Name of depositary institution

The National Collections of Industrial and Marine Bacteria Limited (NCIMB)

Address of depositary institution (including postal code and country)

23 St Machar Drive  
Aberdeen AB2 1RY  
Scotland, UK

Date of deposit  
2 May 1995

Accession Number  
NCIMB 40723

C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet

In respect of all designated states in which such action is possible and to the extent that it is legally permissible under the law of the designated state, it is requested that a sample of the deposited micro-organism be made available only by the issue thereof to an independent expert, in accordance with the relevant patent legislation, e.g. Rule 28(4) EPC, and generally similar provisions *mutatis mutandis* for any other designated state.

## D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)

## E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)

The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")

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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

**A.** The indications made below relate to the microorganism referred to in the description  
on page 17, line 18-19

**B. IDENTIFICATION OF DEPOSIT**

Further deposits are identified on an additional sheet

Name of depositary institution

The National Collections of Industrial and Marine Bacteria Limited (NCIMB)

Address of depositary institution (including postal code and country)

23 St Machar Drive  
Aberdeen AB2 1RY  
Scotland, UK

Date of deposit  
2 May 1995

Accession Number  
NCIMB 40722

**C. ADDITIONAL INDICATIONS** (leave blank if not applicable) This information is continued on an additional sheet

In respect of all designated states in which such action is possible and to the extent that it is legally permissible under the law of the designated state, it is requested that a sample of the deposited micro-organism be made available only by the issue thereof to an independent expert, in accordance with the relevant patent legislation, e.g. Rule 28(4) EPC, and generally similar provisions *mutatis mutandis* for any other designated state.

**D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE** (if the indications are not for all designated States)

**E. SEPARATE FURNISHING OF INDICATIONS** (leave blank if not applicable)

The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")

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